Testosterone signaling and the regulation of spermatogenesis

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Spermatogenesis and male fertility are dependent upon the presence of testosterone in the testis. In the absence of testosterone or the androgen receptor, spermatogenesis does not proceed beyond the meiosis stage. The major cellular target and translator of testosterone signals to developing germ cells is the Sertoli cell. In the Sertoli cell, testosterone signals can be translated directly to changes in gene expression (the classical pathway) or testosterone can activate kinases that may regulate processes required to maintain spermatogenesis (the non-classical pathway). Contributions of the classical and non-classical testosterone signaling pathways to the maintenance of spermatogenesis are discussed. Studies that may further elaborate the mechanisms by with the pathways support spermatogenesis are proposed.

Androgens are essential for male fertility and the maintenance of spermatogenesis. ^{1,2} Testosterone is the androgen in the testis that is responsible for supporting spermatogenesis. In the absence of testosterone or functional androgen receptors (AR), males are infertile because spermatogenesis rarely progresses beyond meiosis. ³⁻⁵

Testosterone is produced by Leydig cells in the interstitial space of the testis. As a result of the local production, testosterone levels in the testis in men are 25 to 125-fold greater in the testis (340 to 2,000 nM) as compared to serum (8.7–35 nM). Testosterone levels are similarly elevated in rodent testes. Thus far, the specific physiologic requirements for high levels of testosterone in the testis are not known. However, it has been established that spermatogenesis does not proceed in the absence of relatively high levels of testosterone (>70 nM in the rat).

Cellular Targets of Testosterone in the Testis

AR is present in the somatic Leydig, peritubular and Sertoli cells. The localization of AR to germ cells is controversial with some studies finding AR positive germ cells and other studies showing that there is no AR in germ cells (reviewed by Wang and colleagues). Functional evidence suggests that if AR is expressed in germ cells it is not required. Specifically, chimeric male mice

Correspondence to: William H. Walker; Email: walkerw@pitt.edu Submitted: 05/31/11; Accepted: 05/31/11 DOI: 10.4161/spmg.1.2.16956 having both AR defective and wild type germ cells produced pups from the AR defective germ cells.¹³ Also, AR defective germ cells transplanted into the testes of azoospermic male mice were able to form colonies of cells undergoing spermatogenesis.¹⁴ Finally, cell-specific knock out of AR in germ cells such that AR is not expressed during or after meiosis did not alter spermatogenesis or fertility indicating that AR is not required in later stage germ cells.¹⁵

Sertoli cells are thought to be the major cellular target for the testosterone signaling that is required to support male germ cell development and survival. AR expression levels rise and fall in adult Sertoli cells in a manner corresponding with the cyclical stages of the seminiferous epithelium. In the rat, the expression of AR protein is low and difficult to detect except during stages VI–VIII when AR levels increase dramatically. AR expression is similarly cyclical in men. It is during stages VI–IX that the lack of testosterone or AR most affects processes required for spermatogenesis. S,20,21

Regulation of Spermatogenesis Control Points by Testosterone and AR

Testosterone deprivation studies performed in rodents have established that testosterone is required for germ cells to progress beyond meiosis and that testosterone is required for the release of mature spermatids during stage VIII in rats (reviewed by Sharpe). Thus far, evidence of direct testosterone support of meiosis is lacking as there are few meiosis-specific processes that are known to be directly regulated by AR-dependent actions. Instead, testosterone may act indirectly to permit germ cells to complete meiosis.

Withdrawal of testosterone or knock out of AR in Sertoli cells results in three major impairments to fertility. First, the integrity of the blood testis barrier (BTB) is compromised, which exposes post meiotic germ cells, formerly in a secluded specialized environment, to autoimmune attack and cytotoxic factors. ^{22,23} Second, there is a block in conversion of round spermatids to elongated spermatids due to a defect in cell adhesion that causes the premature detachment of round spermatids from Sertoli cells. ^{21,24,25} Third, fully mature spermatozoa cannot be released from Sertoli cells and the germ cells are phagocytized by the Sertoli cells. ²¹

The use of Cre-Lox conditional knockout techniques to create mice in which the loss of AR is restricted to Sertoli cells (SCARKO mice) has allowed for a more precise determination of

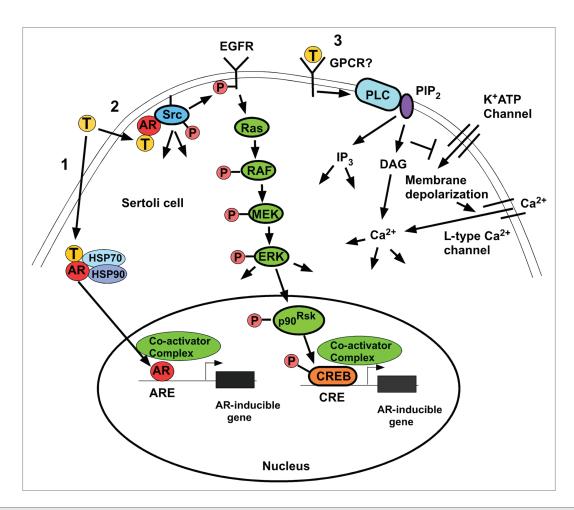


Figure 1. Testosterone signaling pathways. (1) The classical testosterone signaling pathway. Testosterone diffuses through the plasma membrane and binds with the AR. The AR undergoes an alteration in conformation allowing it to be released from heat shock proteins in the cytoplasm. AR then is able to translocate to the nucleus where it binds to specific DNA sequences called androgen response elements (AREs). AR binding to an ARE allows the recruitment of co-activator and co-repressor proteins that alter the expression of genes to alter cellular function. (2) The non-classical kinase activation pathway: testosterone interacts with the classical AR that then is able to recruit and activate Src, which causes the activation of the EGF receptor via an intracellular pathway. The EGF receptor then activates the MAP kinase cascade most likely through Ras resulting in the sequential activation of RAF and MEK and then ERK that activates p90^{Rsk}-kinase, which is known to phosphorylate CREB on serine 133. As a result, CREB-regulated genes such as lactate dehydrogenase A (LDH-A) and early growth response 1 (Egr1) and CREB can be induced by testosterone. (3) The non-classical Ca²⁺ influx pathway: Testosterone interacts with a receptor in the plasma membrane that has characteristics of a G_q coupled G-protein coupled receptor (GPCR). Phospholipase C (PLC) is activated to cleave PIP₂ into IP₃ and DAG. Lower concentrations of PIP₂ inhibit K⁺_{ATP} channels causing membrane depolarization and Ca²⁺ entry via L-type Ca²⁺ channels.

the effects of testosterone action on Sertoli cells in an otherwise normal testis. These strategies determined that, in the absence of Sertoli cell AR, spermatogenesis in mice does not progress beyond the pachytene or diplotene stages of meiosis^{5,15} and the integrity of junctional complexes making up the BTB are not maintained.^{20,26} Specifically, studies of SCARKO mice indicate that androgens regulate the expression levels of BTB tight junction-associated proteins and their localization.²² Studies of cultured Sertoli cells have determined that testosterone stimulation increases the rate at which integral membrane adhesion proteins are endocytosed and then recycled to the membrane suggesting that testosterone may assist in the cyclical reformation of the BTB after the passage of leptotene spermatocytes through the barrier.²⁷ More recent studies have identified AR expression in Sertoli cells as a factor that limits the expression of differentiation markers in

spermatogonial germ cells²⁸ and that Sertoli cell nuclei show signs of immaturity and are abnormally localized away from the basal lamina.^{22,26,28,29} The implications of these last two characteristics of AR deficient Sertoli cells for maintaining spermatogenesis have not yet been investigated.

Classical and Non-Classical Testosterone Actions in Sertoli Cells

The classical testosterone signaling pathway. Testosterone has been shown to act via two pathways: the classical and the non-classical.^{30,31} In the classical pathway (Fig. 1, left), testosterone diffuses through the plasma membrane and binds AR that is sequestered by heat shock proteins in the cytoplasm. A conformational change in AR causes the receptor to be released from

heat shock proteins. AR then translocates to the nucleus where it binds to androgen response elements (AREs) in gene promoter regions, recruits co-regulator proteins and regulates gene transcription. Activation of the classical pathway requires at least 30 to 45 min to initiate changes in gene expression.³²

Several microarray studies using various models have been performed to survey testicular gene expression in the presence and absence of testosterone signaling (reviewed by Verhoeven and colleagues).³³ A broad spectrum of genes in the testis were found to be regulated by testosterone, but the number of Sertoli cell-specific genes that are regulated by testosterone make up a small subset. Furthermore, the genes identified in the microarray studies performed thus far show relatively little overlap and the number of genes displaying a two-fold or greater change in expression are limited.³³ Interestingly, a relatively high percentage of the regulated genes are inhibited by testosterone. Although one study determined that 65% of AR-regulated genes were linked to a conserved ARE within 6 kb of their transcription start sites, only the *Rhox5* (Pem) homeobox transcription factor encoding gene, has been shown to be induced in Sertoli cells by androgens through AR binding to ARE promoter elements.³⁴ Presently, there is no evidence that any one AR-regulated gene is critical for the completion of spermatogenesis; however, it is likely that spermatogenesis would be disrupted as a result of the mutation or elimination of multiple AR-regulated genes.²⁸ Further work is required to characterize the AR-regulated genes regulated by testosterone via the classical pathway as being essential or nonessential for spermatogenesis.

Because testosterone and AR are essential for spermatogenesis and male fertility, it is surprising that the gene survey studies have not identified more testosterone-regulated genes expressed in Sertoli cells that are required for spermatogenesis. One explanation for the lack of identified genes responsible for spermatogenesis may lie in the animal models used to obtain the microarray data. Thus far, gene expression data has been obtained from either prepubertal rats and mice or from AR knock out mice in which AR expression is eliminated before birth. In both models, the testes lack full complements of germ cells, which decreases the complexity of the signals received by Sertoli cells. One solution to the problem may be to selectively knock out AR in Sertoli cells in adult mice and obtain gene expression profiles prior to the loss of germ cells. Fortunately, at least one group is developing an adult mouse model in which the AR gene can be inducibly extinguished.³⁵ Further confirmation of the importance of AR-regulated genes for maintaining fertility in mice may be obtained in the future through comparisons to genetic surveys of mutated genes found in infertile men.

The non-classical testosterone signaling pathway. There are at least two non-classical mechanisms of testosterone action in Sertoli cells. In the testosterone-mediated [Ca²+] influx pathway (Fig. 1, right), testosterone rapidly induces the influx of [Ca²+] into Sertoli cells within 20–40 sec through L-Type [Ca²+] channels. 36,37 Testosterone also is thought to cause the activation of an unidentified $G_{\rm q}$ type G protein coupled receptor and the activation of phospholipase C (PLC) that then hydrolyzes PIP $_{\rm 2}$ in the plasma membrane to produce IP $_{\rm 3}$ and diacylglycerol (DAG). The

decrease in the levels of PIP₂, an inhibitor of ATP-mediated activation of K⁺_{ATP} channels, promotes the closing of these channels causing an increase in membrane resistance and depolarization of the cell. As a result, voltage dependent L-type Ca²⁺ channels open and allow the influx of Ca²⁺, which may alter many cellular processes.³⁸ Thus far, potential cellular targets and spermatogenesis processes regulated by the testosterone-mediated [Ca²⁺] influx pathway have not been investigated.³⁹

Testosterone also has been shown to rapidly activate a series of kinases in Sertoli cells that are known to regulate spermatogenesis. Stimulation of Sertoli cells with levels of testosterone (10-250 nM) that are similar to or lower than those found in the testis causes AR to transiently localize to the plasma membrane and results in AR interacting with and activating Src tyrosine kinase (Fig. 1 and middle). 40 Androgen stimulation triggers the direct association of the proline rich region of AR (amino acids 352-359) and the SH3 domain of Src. 41 Testosterone-mediated activation of Src causes the phosphorylation and stimulation of the EGF receptor (EGFR) via an intracellular pathway. Stimulation of EGFR is required to activate the MAP kinase cascade (Raf, MEK, ERK) that causes p90^{Rsk} kinase to phosphorylate the CREB transcription factor. 40 Activation of the non-classical pathway has been shown to induce the expression of CREB-mediated gene expression. 42 In contrast to the classical pathway, induction of ERK and CREB phosphorylation by testosterone is rapid (within 1 min) and can be sustained for at least 12 hr. 42 The regulation of additional gene expression by other transcription factors downstream of ERK and Src remains to be investigated.

The activation of Src and Erk kinases by non-classical testosterone signaling was found to alter processes that are critical to maintain spermatogenesis. Testosterone stimulation of Sertoli cells co-cultured with germ cells from adult rats increased the numbers of germ cells attached to the Sertoli cells by 50%. However, the addition of inhibitors of Src or ERK kinase reduced germ cell attachment below basal levels. 40 Additional studies were performed in which AR-defective Sertoli cells were infected with adenovirus constructs expressing wild type AR or AR mutants that selectively activated only the classical pathway or the nonclassical pathway. In these studies, testosterone stimulation could only increase the attachment of germ cells to Sertoli cells expressing wild type AR or mutated AR that can stimulate the non-classical pathway. 40 These findings suggest that testosterone can act via the activation of Src and ERK kinases to facilitate Sertoli-germ cell attachment. It is possible that testosterone signaling that increases dramatically in stages VII-VIII of the cycle may be responsible for the remodeling of Sertoli-germ cell adhesion complexes that occurs during these stages when round spermatids begin to elongate. Furthermore, in testosterone deprived or AR deficient Sertoli cells, the lack of non-classical pathwayinduced kinase activation may be responsible for the sloughing off and loss of spermatids that occurs during stages VII-VIII in the absence of testosterone signaling.

The release of mature sperm from Sertoli cells was also shown to be regulated by Src kinase that is activated by non-classical signaling. Seminiferous tubule fragments were micro dissected to isolate fragments containing only stages VII–VIII having mature

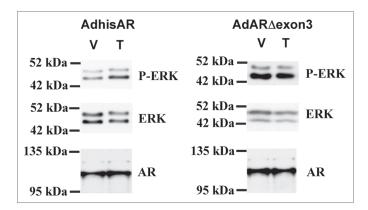


Figure 2. Deletion of exon 3 eliminates non-classical AR activity. 15P-1 Sertoli cells were infected with adenovirus constructs expressing wild type AR (AdhisAR) or exon 3-deleted AR (AdAR Δ exon 3). P-ERK, ERK and AR levels were determined by western blot after a 10 min stimulation in serum free media with vehicle (V) or 100 nM testosterone (T).

elongated spermatids that were ready to be released. Culturing the seminiferous tubule fragments in the presence of a Src kinase inhibitor resulted in the release of 45% fewer sperm. These results are consistent with earlier studies showing that during stages VII–VIII when sperm are released, activated Src levels increase in the vicinity of the specialized Sertoli-elongated spematid adhesion complex called the ectoplasmic specialization (ES). Furthermore, Src is structurally associated with cell adhesion regulatory proteins at the ES. Src also is known to phosphorylate focal adhesion kinase (FAK), β -catenin and N-cadherin proteins that contribute to the formation of the adhesion complexes between Sertoli cells and the mature elongated spermatids. Fig. 45% of a spermatid spermatids.

It has been proposed that only the classical pathway is required for spermatogenesis because spermatogenesis is halted during meiosis in transgenic mice in which exon 3 of the AR containing a portion of the DNA binding domain was removed. However, the non-classical activity of the exon 3-deleted AR mutation was not tested in the study. Recreation of the AR mutant lacking exon 3 and analysis of non-classical testosterone signaling in a Sertoli cell line lacking AR activity revealed that the mutant did not permit the phosphorylation of ERK in response to testosterone stimulation (Fig. 2). This result indicates that the removal of more than 50 amino acids of AR in this model may alter the structure of AR to eliminate both non-classical and classical activity.

Applying Lessons Learned to Future Studies

Work is underway to better characterize the spermatogenesis processes in vivo that are regulated by the classical and non-classical pathways. Transgenic mouse models are being created in which the endogenous AR gene is removed while simultaneously initiating the expression of previously characterized mutant AR genes that are capable of only activating one of the testosterone signaling pathways (Walker WH, unpublished data). Analysis of these mouse models will determine the extent to which spermatogenesis progression is allowed by each of the pathways independently.

Furthermore, the genes that are regulated by each pathway will be identified and the effects of each pathway on the maintenance of the BTB, germ cell adhesion and the release of mature sperm will be determined.

It is likely that both pathways will be found to contribute important independent regulatory actions required to maintain spermatogenesis. Signals from the two pathways also may act in concert or synergy. Data obtained from studies of progesterone, glucocorticoid and estrogen receptor function suggest that the classical and non-classical pathways cross-talk and interact in their target cells. Specifically, stimulation of cells with the steroid hormones resulted in rapid phosphorylation of their cognate receptors, which permitted the receptor to recruit co-factors resulting in the increased stimulation of specific endogenous target genes.^{51,52} Also, rapid signaling through AR has been shown to phosphorylate paxillin, which was found to contribute to testosterone-mediated transcription in prostate cells.⁵³ It is possible that the phosphorylation and activation of kinases by the nonclassical pathway in Sertoli cells may contribute to gene expression regulation via the classical pathway. In addition, important gene targets may be regulated independently downstream of the kinases that are activated via the non-classical pathway as exemplified by the androgen-mediated activation of the CREB transcription factor that is required for spermatogenesis. 42,54

If the non-classical pathway is found to be required to maintain spermatogenesis, then it is expected that new targets for the regulation of spermatogenesis will be identified. One potential target for contraceptive development could be the testosterone-induced interaction of AR and Src kinase that initiates the non-classical pathway. Peptides that have already been identified to block AR-Src interactions^{55,56} and corresponding peptidomimetic molecules are being assessed for blocking the non-classical pathway and spermatogenesis (Walker WH, unpublished data). It is possible that the partnering of factors that block the non-classical pathway with a Sertoli cell-specific delivery system could provide a hormone independent, reversible male contraceptive.

Conclusion

Although testosterone has been known to be essential for male fertility for at least 70 years, ^{57,58} the molecular mechanisms by which testosterone acts to support spermatogenesis are only now being identified. The identification of testosterone-regulated genes and kinases in Sertoli cells has allowed for the discovery of the precise targets of testosterone action and a better understanding of the how testosterone regulates the process of spermatogenesis. As the molecular mechanisms of testosterone signaling continue to be revealed, we will accumulate the intellectual resources required to produce therapies for specific male infertility conditions and targets for contraceptive development.

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